1: AJ242651. Reports Hepatitis C virus...[gi:5441831] Links

Features Sequence

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DEFINITION  Hepatitis C virus replicon I377/NS2-3'UTR.
ACCESSION   AJ242651
VERSION     AJ242651.1  GI:5441831
KEYWORDS    core-neo gene; NS2 gene; NS2 proteinase; NS3 gene; NS3
            proteinase/helicase; NS3/4A proteinase cofactor; NS4A gene; NS4B
            gene; NS4b protein; NS5a gene; NS5A phosphoprotein; NS5b gene; NS5B
            RNA dependant RNA polymerase; polyprotein.
SOURCE      Hepatitis C virus replicon I377/NS2-3'UTR
  ORGANISM  Hepatitis C virus replicon I377/NS2-3'UTR
            other sequences; artificial sequences; vectors.
REFERENCE   1
  AUTHORS   Lohmann,V., Korner,F., Koch,J., Herian,U., Theilmann,L. and
            Bartenschlager,R.
  TITLE     Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell
            line
  JOURNAL   Science 285 (5424), 110-113 (1999)
   PUBMED   10390360
REFERENCE   2  (bases 1 to 8637)
  AUTHORS   Bartenschlager,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology,
            Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67,
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Blast 2 Sequences results

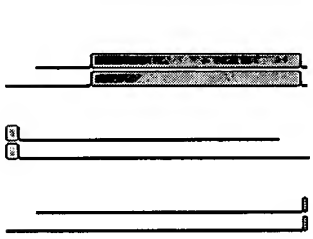
PubMed Entrez BLAST OMIM Taxonomy Structure

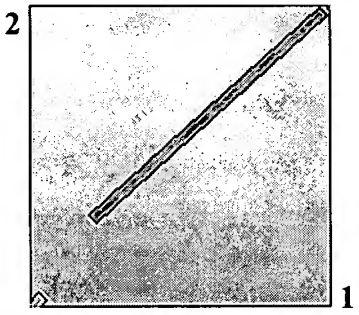
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.17 [Aug-26-2007]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 0 expect: 10.0000 wordsize: 11 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|5441831|Hepatitis C virus replicon I377/NS2-3'UTR
Length = 8636 (1 .. 8637)

Sequence 2: gi|5420376|Hepatitis C virus type 1b complete genome, isolate Con1
Length = 9605 (1 .. 9605)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

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 Score = 1.261e+04 bits (6560),  Expect = 0.0
 Identities = 6646/6646 (100%), Gaps = 0/6646 (0%)
 Strand=Plus/Plus

Query  1799  CCATGGACCGGGAGATGGCAGCATCGTGCGGAGGCGCGGTTTTCGTAGGTCTGATACTCT  1858
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2767  CCATGGACCGGGAGATGGCAGCATCGTGCGGAGGCGCGGTTTTCGTAGGTCTGATACTCT  2826

Query  1859  TGACCTTGTCACCGCACTATAAGCTGTTCCTCGCTAGGCTCATATGGTGGTTACAATATT  1918
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2827  TGACCTTGTCACCGCACTATAAGCTGTTCCTCGCTAGGCTCATATGGTGGTTACAATATT  2886

Query  1919  TTATCACCAGGGCCGAGGCACACTTGCAAGTGTGGATCCCCCCCCCTCAACGTTCGGGGGG  1978
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  2887  TTATCACCAGGGCCGAGGCACACTTGCAAGTGTGGATCCCCCCCCCTCAACGTTCGGGGGG  2946

Query  1979  GCCGCGATGCCGTCATCCTCCTCACGTGCGCGATCCACCCAGAGCTAATCTTTACCATCA  2038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2947  GCCGCGATGCCGTCATCCTCCTCACGTGCGCGATCCACCCAGAGCTAATCTTTACCATCA  3006

Query  2039  CCAAAATCTTGCTCGCCATACTCGGTCCACTCATGGTGCTCCAGGCTGGTATAACCAAAG  2098
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Sbjct  3007  CCAAAATCTTGCTCGCCATACTCGGTCCACTCATGGTGCTCCAGGCTGGTATAACCAAAG  3066

Query  2099  TGCCGTACTTCGTGCGCGCACACGGGCTCATTCGTGCATGCATGCTGGTGCGGAAGGTTG  2158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3067  TGCCGTACTTCGTGCGCGCACACGGGCTCATTCGTGCATGCATGCTGGTGCGGAAGGTTG  3126

Query  2159  CTGGGGGTCATTATGTCCAAATGGCTCTCATGAAGTTGGCCGCACTGACAGGTACGTACG  2218
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Sbjct  3127  CTGGGGGTCATTATGTCCAAATGGCTCTCATGAAGTTGGCCGCACTGACAGGTACGTACG  3186

Query  2219  TTTATGACCATCTCACCCCACTGCGGGACTGGGCCCACGCGGGCCTACGAGACCTTGCGG  2278
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Sbjct  3187  TTTATGACCATCTCACCCCACTGCGGGACTGGGCCCACGCGGGCCTACGAGACCTTGCGG  3246

Query  2279  TGGCAGTTGAGCCCGTCGTCTTCTCTGATATGGAGACCAAGGTTATCACCTGGGGGGCAG  2338
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Sbjct  3247  TGGCAGTTGAGCCCGTCGTCTTCTCTGATATGGAGACCAAGGTTATCACCTGGGGGGCAG  3306

Query  2339  ACACCGCGGCGTGTGGGGACATCATCTTGGGCCTGCCCGTCTCCGCCCGCAGGGGGAGGG  2398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3307  ACACCGCGGCGTGTGGGGACATCATCTTGGGCCTGCCCGTCTCCGCCCGCAGGGGGAGGG  3366

Query  2399  AGATACATCTGGGACCGGCAGACAGCCTTGAAGGGCAGGGGTGGCGACTCCTCGCGCCTA  2458
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Sbjct  3367  AGATACATCTGGGACCGGCAGACAGCCTTGAAGGGCAGGGGTGGCGACTCCTCGCGCCTA  3426

Query  2459  TTACGGCCTACTCCCAACAGACGCGAGGCCTACTTGGCTGCATCATCACTAGCCTCACAG  2518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3427  TTACGGCCTACTCCCAACAGACGCGAGGCCTACTTGGCTGCATCATCACTAGCCTCACAG  3486

Query  2519  GCCGGGACAGGAACCAGGTCGAGGGGGAGGTCCAAGTGGTCTCCACCGCAACACAATCTT  2578
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Sbjct  3487  GCCGGGACAGGAACCAGGTCGAGGGGGAGGTCCAAGTGGTCTCCACCGCAACACAATCTT  3546

Query  2579  TCCTGGCGACCTGCGTCAATGGCGTGTGTTGGACTGTCTATCATGGTGCCGGCTCAAAGA  2638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3547  TCCTGGCGACCTGCGTCAATGGCGTGTGTTGGACTGTCTATCATGGTGCCGGCTCAAAGA  3606

Query  2639  CCCTTGCCGGCCCAAAGGGCCCAATCACCCAAATGTACACCAATGTGGACCAGGACCTCG  2698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3607  CCCTTGCCGGCCCAAAGGGCCCAATCACCCAAATGTACACCAATGTGGACCAGGACCTCG  3666

Query  2699  TCGGCTGGCAAGCGCCCCCCGGGGCGCGTTCCTTGACACCATGCACCTGCGGCAGCTCGG  2758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3667  TCGGCTGGCAAGCGCCCCCCGGGGCGCGTTCCTTGACACCATGCACCTGCGGCAGCTCGG  3726

Query  2759  ACCTTTACTTGGTCACGAGGCATGCCGATGTCATTCCGGTGCGCCGGCGGGGCGACAGCA  2818
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Sbjct  3727  ACCTTTACTTGGTCACGAGGCATGCCGATGTCATTCCGGTGCGCCGGCGGGGCGACAGCA  3786

Query  2819  GGGGGAGCCTACTCTCCCCCAGGCCCGTCTCCTACTTGAAGGGCTCTTCGGGCGGTCCAC  2878
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Sbjct  3787  GGGGGAGCCTACTCTCCCCCAGGCCCGTCTCCTACTTGAAGGGCTCTTCGGGCGGTCCAC  3846

Query  2879  TGCTCTGCCCCTCGGGGCACGCTGTGGGCATCTTTCGGGCTGCCGTGTGCACCCGAGGGG  2938
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Sbjct  3847  TGCTCTGCCCCTCGGGGCACGCTGTGGGCATCTTTCGGGCTGCCGTGTGCACCCGAGGGG  3906

Query  2939  TTGCGAAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTATGCGGTCCCCGG  2998
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Sbjct  3907  TTGCGAAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTATGCGGTCCCCGG  3966

Query  2999  TCTTCACGGACAACTCGTCCCCTCCGGCCGTACCGCAGACATTCCAGGTGGCCCATCTAC  3058
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Sbjct  3967  TCTTCACGGACAACTCGTCCCCTCCGGCCGTACCGCAGACATTCCAGGTGGCCCATCTAC  4026

Query  3059  ACGCCCCTACTGGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCGTATGCAGCCCAAGGGT  3118
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Sbjct  4027  ACGCCCCTACTGGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCGTATGCAGCCCAAGGGT  4086

Query  3119  ATAAGGTGCTTGTCCTGAACCCGTCCGTCGCCGCCACCCTAGGTTTCGGGGCGTATATGT  3178
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Sbjct  4087  ATAAGGTGCTTGTCCTGAACCCGTCCGTCGCCGCCACCCTAGGTTTCGGGGCGTATATGT  4146

Query  3179  CTAAGGCACATGGTATCGACCCTAACATCAGAACCGGGGTAAGGACCATCACCACGGGTG  3238
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Sbjct  4147  CTAAGGCACATGGTATCGACCCTAACATCAGAACCGGGGTAAGGACCATCACCACGGGTG  4206

Query  3239  CCCCCATCACGTACTCCACCTATGGCAAGTTTCTTGCCGACGGTGGTTGCTCTGGGGGCG  3298
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Sbjct  4207  CCCCCATCACGTACTCCACCTATGGCAAGTTTCTTGCCGACGGTGGTTGCTCTGGGGGCG  4266

Query  3299  CCTATGACATCATAATATGTGATGAGTGCCACTCAACTGACTCGACCACTATCCTGGGCA  3358
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Sbjct  4267  CCTATGACATCATAATATGTGATGAGTGCCACTCAACTGACTCGACCACTATCCTGGGCA  4326

Query  3359  TCGGCACAGTCCTGGACCAAGCGGAGACGGCTGGAGCGCGACTCGTCGTGCTCGCCACCG  3418
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Query  3419  CTACGCCTCCGGGATCGGTCACCGTGCCACATCCAAACATCGAGGAGGTGGCTCTGTCCA  3478
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Sbjct  4387  CTACGCCTCCGGGATCGGTCACCGTGCCACATCCAAACATCGAGGAGGTGGCTCTGTCCA  4446

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Sbjct  4447  GCACTGGAGAAATCCCCTTTTATGGCAAAGCCATCCCCATCGAGACCATCAAGGGGGGGA  4506

Query  3539  GGCACCTCATTTTCTGCCATTCCAAGAAGAAATGTGATGAGCTCGCCGCGAAGCTGTCCG  3598
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Sbjct  4507  GGCACCTCATTTTCTGCCATTCCAAGAAGAAATGTGATGAGCTCGCCGCGAAGCTGTCCG  4566

Query  3599  GCCTCGGACTCAATGCTGTAGCATATTACCGGGGCCTTGATGTATCCGTCATACCAACTA  3658
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Sbjct  4567  GCCTCGGACTCAATGCTGTAGCATATTACCGGGGCCTTGATGTATCCGTCATACCAACTA  4626

Query  3659  GCGGAGACGTCATTGTCGTAGCAACGGACGCTCTAATGACGGGCTTTACCGGCGATTTCG  3718
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Sbjct  4627  GCGGAGACGTCATTGTCGTAGCAACGGACGCTCTAATGACGGGCTTTACCGGCGATTTCG  4686

Query  3719  ACTCAGTGATCGACTGCAATACATGTGTCACCCAGACAGTCGACTTCAGCCTGGACCCGA  3778
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Sbjct  4687  ACTCAGTGATCGACTGCAATACATGTGTCACCCAGACAGTCGACTTCAGCCTGGACCCGA  4746

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Sbjct  4747  CCTTCACCATTGAGACGACGACCGTGCCACAAGACGCGGTGTCACGCTCGCAGCGGCGAG  4806

Query  3839  GCAGGACTGGTAGGGGCAGGATGGGCATTTACAGGTTTGTGACTCCAGGAGAACGGCCCT  3898
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Sbjct  4807  GCAGGACTGGTAGGGGCAGGATGGGCATTTACAGGTTTGTGACTCCAGGAGAACGGCCCT  4866

Query  3899  CGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGCTATGACGCGGGCTGTGCTTGGTACG  3958
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Sbjct  4867  CGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGCTATGACGCGGGCTGTGCTTGGTACG  4926

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Sbjct  4927  AGCTCACGCCCGCCGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACACCAGGGTTGC  4986

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Sbjct  4987  CCGTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCCTCACCCACATAG  5046

Query  4079  ACGCCCATTTCTTGTCCCAGACTAAGCAGGCAGGAGACAACTTCCCCTACCTGGTAGCAT  4138
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Sbjct  5047  ACGCCCATTTCTTGTCCCAGACTAAGCAGGCAGGAGACAACTTCCCCTACCTGGTAGCAT  5106

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Sbjct  5107  ACCAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCATCGTGGGACCAAATGTGGA  5166

Query  4199  AGTGTCTCATACGGCTAAAGCCTACGCTGCACGGGCCAACGCCCCTGCTGTATAGGCTGG  4258
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Sbjct  5167  AGTGTCTCATACGGCTAAAGCCTACGCTGCACGGGCCAACGCCCCTGCTGTATAGGCTGG  5226

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Sbjct  5287  TGTCGGCTGACCTGGAGGTCGTCACGAGCACCTGGGTGCTGGTAGGCGGAGTCCTAGCAG  5346

Query  4379  CTCTGGCCGCGTATTGCCTGACAACAGGCAGCGTGGTCATTGTGGGCAGGATCATCTTGT  4438
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Sbjct  5347  CTCTGGCCGCGTATTGCCTGACAACAGGCAGCGTGGTCATTGTGGGCAGGATCATCTTGT  5406

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Sbjct  5407  CCGGAAAGCCGGCCATCATTCCCGACAGGGAAGTCCTTTACCGGGAGTTCGATGAGATGG  5466

Query  4499  AAGAGTGCGCCTCACACCTCCCTTACATCGAACAGGGAATGCAGCTCGCCGAACAATTCA  4558
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Sbjct  5467  AAGAGTGCGCCTCACACCTCCCTTACATCGAACAGGGAATGCAGCTCGCCGAACAATTCA  5526

Query  4559  AACAGAAGGCAATCGGGTTGCTGCAAACAGCCACCAAGCAAGCGGAGGCTGCTGCTCCCG  4618
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Sbjct  5527  AACAGAAGGCAATCGGGTTGCTGCAAACAGCCACCAAGCAAGCGGAGGCTGCTGCTCCCG  5586

Query  4619  TGGTGGAATCCAAGTGGCGGACCCTCGAAGCCTTCTGGGCGAAGCATATGTGGAATTTCA  4678
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Sbjct  5587  TGGTGGAATCCAAGTGGCGGACCCTCGAAGCCTTCTGGGCGAAGCATATGTGGAATTTCA  5646

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Sbjct  5647  TCAGCGGGATACAATATTTAGCAGGCTTGTCCACTCTGCCTGGCAACCCCGCGATAGCAT  5706

Query  4739  CACTGATGGCATTCACAGCCTCTATCACCAGCCCGCTCACCACCCAACATACCCTCCTGT  4798
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Sbjct  5707  CACTGATGGCATTCACAGCCTCTATCACCAGCCCGCTCACCACCCAACATACCCTCCTGT  5766

Query  4799  TTAACATCCTGGGGGGATGGGTGGCCGCCCAACTTGCTCCTCCCAGCGCTGCTTCTGCTT  4858
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Sbjct  5767  TTAACATCCTGGGGGGATGGGTGGCCGCCCAACTTGCTCCTCCCAGCGCTGCTTCTGCTT  5826

Query  4859  TCGTAGGCGCCGGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCCTTGGGAAGGTGCTTG  4918
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Sbjct  5827  TCGTAGGCGCCGGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCCTTGGGAAGGTGCTTG  5886

Query  4919  TGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCGCTCGTGGCCTTTAAGGTCA  4978
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Sbjct  5887  TGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCGCTCGTGGCCTTTAAGGTCA  5946

Query  4979  TGAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACCTACTCCCTGCTATCCTCTCCC  5038
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Sbjct  5947  TGAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACCTACTCCCTGCTATCCTCTCCC  6006

Query  5039  CTGGCGCCCTAGTCGTCGGGGTCGTGTGCGCAGCGATACTGCGTCGGCACGTGGGCCCAG  5098
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Sbjct  6007  CTGGCGCCCTAGTCGTCGGGGTCGTGTGCGCAGCGATACTGCGTCGGCACGTGGGCCCAG  6066

Query  5099  GGGAGGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTCGCTTCGCGGGGTAACCACG  5158
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Sbjct  6067  GGGAGGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTCGCTTCGCGGGGTAACCACG  6126

Query  5159  TCTCCCCCACGCACTATGTGCCTGAGAGCGACGCTGCAGCACGTGTCACTCAGATCCTCT  5218
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Query  5219  CTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCACCAGTGGATCAACGAGGACTGCT  5278
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Sbjct  6187  CTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCACCAGTGGATCAACGAGGACTGCT  6246

Query  5279  CCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTGGATATGCACGGTGTTGA  5338
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Sbjct  6247  CCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTGGATATGCACGGTGTTGA  6306

Query  5339  CTGATTTCAAGACCTGGCTCCAGTCCAAGCTCCTGCCGCGATTGCCGGGAGTCCCCTTCT  5398
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Sbjct  6307  CTGATTTCAAGACCTGGCTCCAGTCCAAGCTCCTGCCGCGATTGCCGGGAGTCCCCTTCT  6366

Query  5399  TCTCATGTCAACGTGGGTACAAGGGAGTCTGGCGGGGCGACGGCATCATGCAAACCACCT  5458
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Sbjct  6367  TCTCATGTCAACGTGGGTACAAGGGAGTCTGGCGGGGCGACGGCATCATGCAAACCACCT  6426

Query  5459  GCCCATGTGGAGCACAGATCACCGGACATGTGAAAAACGGTTCCATGAGGATCGTGGGGC  5518
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Sbjct  6427  GCCCATGTGGAGCACAGATCACCGGACATGTGAAAAACGGTTCCATGAGGATCGTGGGGC  6486

Query  5519  CTAGGACCTGTAGTAACACGTGGCATGGAACATTCCCCATTAACGCGTACACCACGGGCC  5578
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Sbjct  6487  CTAGGACCTGTAGTAACACGTGGCATGGAACATTCCCCATTAACGCGTACACCACGGGCC  6546

Query  5579  CCTGCACGCCCTCCCCGGCGCCAAATTATTCTAGGGCGCTGTGGCGGGTGGCTGCTGAGG  5638
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Sbjct  6547  CCTGCACGCCCTCCCCGGCGCCAAATTATTCTAGGGCGCTGTGGCGGGTGGCTGCTGAGG  6606

Query  5639  AGTACGTGGAGGTTACGCGGGTGGGGGATTTCCACTACGTGACGGGCATGACCACTGACA  5698
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Sbjct  6607  AGTACGTGGAGGTTACGCGGGTGGGGGATTTCCACTACGTGACGGGCATGACCACTGACA  6666

Query  5699  ACGTAAAGTGCCCGTGTCAGGTTCCGGCCCCCGAATTCTTCACAGAAGTGGATGGGGTGC  5758
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Sbjct  6667  ACGTAAAGTGCCCGTGTCAGGTTCCGGCCCCCGAATTCTTCACAGAAGTGGATGGGGTGC  6726

Query  5759  GGTTGCACAGGTACGCTCCAGCGTGCAAACCCCTCCTACGGGAGGAGGTCACATTCCTGG  5818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6727  GGTTGCACAGGTACGCTCCAGCGTGCAAACCCCTCCTACGGGAGGAGGTCACATTCCTGG  6786

Query  5819  TCGGGCTCAATCAATACCTGGTTGGGTCACAGCTCCCATGCGAGCCCGAACCGGACGTAG  5878
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Sbjct  6787  TCGGGCTCAATCAATACCTGGTTGGGTCACAGCTCCCATGCGAGCCCGAACCGGACGTAG  6846

Query  5879  CAGTGCTCACTTCCATGCTCACCGACCCCTCCCACATTACGGCGGAGACGGCTAAGCGTA  5938
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Sbjct  6847  CAGTGCTCACTTCCATGCTCACCGACCCCTCCCACATTACGGCGGAGACGGCTAAGCGTA  6906

Query  5939  GGCTGGCCAGGGGATCTCCCCCCTCCTTGGCCAGCTCATCAGCTAGCCAGCTGTCTGCGC  5998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6907  GGCTGGCCAGGGGATCTCCCCCCTCCTTGGCCAGCTCATCAGCTAGCCAGCTGTCTGCGC  6966

Query  5999  CTTCCTTGAAGGCAACATGCACTACCCGTCATGACTCCCCGGACGCTGACCTCATCGAGG  6058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6967  CTTCCTTGAAGGCAACATGCACTACCCGTCATGACTCCCCGGACGCTGACCTCATCGAGG  7026

Query  6059  CCAACCTCCTGTGGCGGCAGGAGATGGGCGGGAACATCACCCGCGTGGAGTCAGAAAATA  6118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7027  CCAACCTCCTGTGGCGGCAGGAGATGGGCGGGAACATCACCCGCGTGGAGTCAGAAAATA  7086

Query  6119  AGGTAGTAATTTTGGACTCTTTCGAGCCGCTCCAAGCGGAGGAGGATGAGAGGGAAGTAT  6178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7087  AGGTAGTAATTTTGGACTCTTTCGAGCCGCTCCAAGCGGAGGAGGATGAGAGGGAAGTAT  7146

Query  6179  CCGTTCCGGCGGAGATCCTGCGGAGGTCCAGGAAATTCCCTCGAGCGATGCCCATATGGG  6238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7147  CCGTTCCGGCGGAGATCCTGCGGAGGTCCAGGAAATTCCCTCGAGCGATGCCCATATGGG  7206

Query  6239  CACGCCCGGATTACAACCCTCCACTGTTAGAGTCCTGGAAGGACCCGGACTACGTCCCTC  6298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7207  CACGCCCGGATTACAACCCTCCACTGTTAGAGTCCTGGAAGGACCCGGACTACGTCCCTC  7266

Query  6299  CAGTGGTACACGGGTGTCCATTGCCGCCTGCCAAGGCCCCTCCGATACCACCTCCACGGA  6358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7267  CAGTGGTACACGGGTGTCCATTGCCGCCTGCCAAGGCCCCTCCGATACCACCTCCACGGA  7326

Query  6359  GGAAGAGGACGGTTGTCCTGTCAGAATCTACCGTGTCTTCTGCCTTGGCGGAGCTCGCCA  6418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7327  GGAAGAGGACGGTTGTCCTGTCAGAATCTACCGTGTCTTCTGCCTTGGCGGAGCTCGCCA  7386

Query  6419  CAAAGACCTTCGGCAGCTCCGAATCGTCGGCCGTCGACAGCGGCACGGCAACGGCCTCTC  6478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  7387  CAAAGACCTTCGGCAGCTCCGAATCGTCGGCCGTCGACAGCGGCACGGCAACGGCCTCTC  7446

Query  6479  CTGACCAGCCCTCCGACGACGGCGACGCGGGATCCGACGTTGAGTCGTACTCCTCCATGC  6538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7447  CTGACCAGCCCTCCGACGACGGCGACGCGGGATCCGACGTTGAGTCGTACTCCTCCATGC  7506

Query  6539  CCCCCCTTGAGGGGGAGCCGGGGGATCCCGATCTCAGCGACGGGTCTTGGTCTACCGTAA  6598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7507  CCCCCCTTGAGGGGGAGCCGGGGGATCCCGATCTCAGCGACGGGTCTTGGTCTACCGTAA  7566

Query  6599  GCGAGGAGGCTAGTGAGGACGTCGTCTGCTGCTCGATGTCCTACACATGGACAGGCGCCC  6658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7567  GCGAGGAGGCTAGTGAGGACGTCGTCTGCTGCTCGATGTCCTACACATGGACAGGCGCCC  7626

Query  6659  TGATCACGCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTGAGCAACTCTT  6718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7627  TGATCACGCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTGAGCAACTCTT  7686

Query  6719  TGCTCCGTCACCACAACTTGGTCTATGCTACAACATCTCGCAGCGCAAGCCTGCGGCAGA  6778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7687  TGCTCCGTCACCACAACTTGGTCTATGCTACAACATCTCGCAGCGCAAGCCTGCGGCAGA  7746

Query  6779  AGAAGGTCACCTTTGACAGACTGCAGGTCCTGGACGACCACTACCGGGACGTGCTCAAGG  6838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7747  AGAAGGTCACCTTTGACAGACTGCAGGTCCTGGACGACCACTACCGGGACGTGCTCAAGG  7806

Query  6839  AGATGAAGGCGAAGGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAGGAAGCCTGTA  6898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7807  AGATGAAGGCGAAGGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAGGAAGCCTGTA  7866

Query  6899  AGCTGACGCCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGGCAAAGGACGTCCGGA  6958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7867  AGCTGACGCCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGGCAAAGGACGTCCGGA  7926

Query  6959  ACCTATCCAGCAAGGCCGTTAACCACATCCGCTCCGTGTGGAAGGACTTGCTGGAAGACA  7018
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7927  ACCTATCCAGCAAGGCCGTTAACCACATCCGCTCCGTGTGGAAGGACTTGCTGGAAGACA  7986

Query  7019  CTGAGACACCAATTGACACCACCATCATGGCAAAAAATGAGGTTTTCTGCGTCCAACCAG  7078
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7987  CTGAGACACCAATTGACACCACCATCATGGCAAAAAATGAGGTTTTCTGCGTCCAACCAG  8046

Query  7079  AGAAGGGGGGCCGCAAGCCAGCTCGCCTTATCGTATTCCCAGATTTGGGGGTTCGTGTGT  7138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8047  AGAAGGGGGGCCGCAAGCCAGCTCGCCTTATCGTATTCCCAGATTTGGGGGTTCGTGTGT  8106

Query  7139  GCGAGAAAATGGCCCTTTACGATGTGGTCTCCACCCTCCCTCAGGCCGTGATGGGCTCTT  7198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8107  GCGAGAAAATGGCCCTTTACGATGTGGTCTCCACCCTCCCTCAGGCCGTGATGGGCTCTT  8166

Query  7199  CATACGGATTCCAATACTCTCCTGGACAGCGGGTCGAGTTCCTGGTGAATGCCTGGAAAG  7258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8167  CATACGGATTCCAATACTCTCCTGGACAGCGGGTCGAGTTCCTGGTGAATGCCTGGAAAG  8226

Query  7259  CGAAGAAATGCCCTATGGGCTTCGCATATGACACCCGCTGTTTTGACTCAACGGTCACTG  7318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8227  CGAAGAAATGCCCTATGGGCTTCGCATATGACACCCGCTGTTTTGACTCAACGGTCACTG  8286

Query  7319  AGAATGACATCCGTGTTGAGGAGTCAATCTACCAATGTTGTGACTTGGCCCCCGAAGCCA  7378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  8287  AGAATGACATCCGTGTTGAGGAGTCAATCTACCAATGTTGTGACTTGGCCCCCGAAGCCA  8346

Query  7379  GACAGGCCATAAGGTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTGACTAATTCTA  7438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8347  GACAGGCCATAAGGTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTGACTAATTCTA  8406

Query  7439  AAGGGCAGAACTGCGGCTATCGCCGGTGCCGCGCGAGCGGTGTACTGACGACCAGCTGCG  7498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8407  AAGGGCAGAACTGCGGCTATCGCCGGTGCCGCGCGAGCGGTGTACTGACGACCAGCTGCG  8466

Query  7499  GTAATACCCTCACATGTTACTTGAAGGCCGCTGCGGCCTGTCGAGCTGCGAAGCTCCAGG  7558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8467  GTAATACCCTCACATGTTACTTGAAGGCCGCTGCGGCCTGTCGAGCTGCGAAGCTCCAGG  8526

Query  7559  ACTGCACGATGCTCGTATGCGGAGACGACCTTGTCGTTATCTGTGAAAGCGCGGGGACCC  7618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8527  ACTGCACGATGCTCGTATGCGGAGACGACCTTGTCGTTATCTGTGAAAGCGCGGGGACCC  8586

Query  7619  AAGAGGACGAGGCGAGCCTACGGGCCTTCACGGAGGCTATGACTAGATACTCTGCCCCCC  7678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8587  AAGAGGACGAGGCGAGCCTACGGGCCTTCACGGAGGCTATGACTAGATACTCTGCCCCCC  8646

Query  7679  CTGGGGACCCGCCCAAACCAGAATACGACTTGGAGTTGATAACATCATGCTCCTCCAATG  7738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8647  CTGGGGACCCGCCCAAACCAGAATACGACTTGGAGTTGATAACATCATGCTCCTCCAATG  8706

Query  7739  TGTCAGTCGCGCACGATGCATCTGGCAAAAGGGTGTACTATCTCACCCGTGACCCCACCA  7798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8707  TGTCAGTCGCGCACGATGCATCTGGCAAAAGGGTGTACTATCTCACCCGTGACCCCACCA  8766

Query  7799  CCCCCCTTGCGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAATTCCTGGCTAG  7858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8767  CCCCCCTTGCGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAATTCCTGGCTAG  8826

Query  7859  GCAACATCATCATGTATGCGCCCACCTTGTGGGCAAGGATGATCCTGATGACTCATTTCT  7918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8827  GCAACATCATCATGTATGCGCCCACCTTGTGGGCAAGGATGATCCTGATGACTCATTTCT  8886

Query  7919  TCTCCATCCTTCTAGCTCAGGAACAACTTGAAAAAGCCCTAGATTGTCAGATCTACGGGG  7978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8887  TCTCCATCCTTCTAGCTCAGGAACAACTTGAAAAAGCCCTAGATTGTCAGATCTACGGGG  8946

Query  7979  CCTGTTACTCCATTGAGCCACTTGACCTACCTCAGATCATTCAACGACTCCATGGCCTTA  8038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8947  CCTGTTACTCCATTGAGCCACTTGACCTACCTCAGATCATTCAACGACTCCATGGCCTTA  9006

Query  8039  GCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATGCCTCA  8098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9007  GCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATGCCTCA  9066

Query  8099  GGAAACTTGGGGTACCGCCCTTGCGAGTCTGGAGACATCGGGCCAGAAGTGTCCGCGCTA  8158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9067  GGAAACTTGGGGTACCGCCCTTGCGAGTCTGGAGACATCGGGCCAGAAGTGTCCGCGCTA  9126

Query  8159  GGCTACTGTCCCAGGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTCAACTGGGCAG  8218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9127  GGCTACTGTCCCAGGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTCAACTGGGCAG  9186

Query  8219  TAAGGACCAAGCTCAAACTCACTCCAATCCCGGCTGCGTCCCAGTTGGATTTATCCAGCT  8278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  9187  TAAGGACCAAGCTCAAACTCACTCCAATCCCGGCTGCGTCCCAGTTGGATTTATCCAGCT  9246

Query  8279  GGTTCGTTGCTGGTTACAGCGGGGGAGACATATATCACAGCCTGTCTCGTGCCCGACCCC  8338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9247  GGTTCGTTGCTGGTTACAGCGGGGGAGACATATATCACAGCCTGTCTCGTGCCCGACCCC  9306

Query  8339  GCTGGTTCATGTGGTGCCTACTCCTACTTTCTGTAGGGGTAGGCATCTATCTACTCCCCA  8398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9307  GCTGGTTCATGTGGTGCCTACTCCTACTTTCTGTAGGGGTAGGCATCTATCTACTCCCCA  9366

Query  8399  ACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTG  8444
              |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9367  ACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTG  9412
```

Score = 696 bits (362), Expect = 0.0
Identities = 376/376 (100%), Gaps = 0/376 (0%)
Strand=Plus/Plus

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Query  2    CCAGCCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCCTGTGAGGAACTACTGT  61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2    CCAGCCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCCTGTGAGGAACTACTGT  61

Query  62   CTTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACC  121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  62   CTTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACC  121

Query  122  CCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGG  181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  122  CCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGG  181

Query  182  ACGACCGGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCG  241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  182  ACGACCGGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCG  241

Query  242  CGAGACTGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGG  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  242  CGAGACTGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGG  301

Query  302  TGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACC  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  302  TGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACC  361

Query  362  TCAAAGAAAAACCAAA  377
            ||||||||||||||||
Sbjct  362  TCAAAGAAAAACCAAA  377
```

Score = 189 bits (98), Expect = 2e-43
Identities = 98/98 (100%), Gaps = 0/98 (0%)

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 Strand=Plus/Plus

Query  8540  GGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAAGGTCCGTGAGCCGCTTGACT  8599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9508  GGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAAGGTCCGTGAGCCGCTTGACT  9567

Query  8600  GCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCAAGT  8637
             ||||||||||||||||||||||||||||||||||||||
Sbjct  9568  GCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCAAGT  9605


CPU time:      0.12 user secs.       0.04 sys. secs          0.16 total secs.
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